

Shin-Lin Chen



OIPF

RAW SEQUENCE LISTING

DATE: 05/19/2003

PATENT APPLICATION: US/09/925,548A

TIME: 11:18:37

Input Set : D:\seqlist.txt

Output Set: N:\CRF4\05192003\I925548A.raw

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4 1100 APPLICANT: Dedhar, Shukat
5      Hannigan, Greg
6      Yee, Arthur
8 1200 TITLE OF INVENTION: INTEGRIN-LINKED KINASE AND ITS USES
11 1300 FILE REFERENCE: KINE001CIE4
12 1400 CURRENT APPLICATION NUMBER: 09/925,548A
14 1410 CURRENT FILING DATE: 2001-08-08
16 1500 PRIOR APPLICATION NUMBER: 04/390,425
17 1510 PRIOR FILING DATE: 1999-09-03
19 1500 PRIOR APPLICATION NUMBER: 09/015,706
20 1510 PRIOR FILING DATE: 1998-03-05
22 1500 PRIOR APPLICATION NUMBER: 08/915,841
23 1510 PRIOR FILING DATE: 1997-10-31
25 1500 PRIOR APPLICATION NUMBER: 08/782,345
26 1510 PRIOR FILING DATE: 1996-11-19
28 1500 PRIOR APPLICATION NUMBER: 69/009,074
29 1510 PRIOR FILING DATE: 1995-12-21
31 1600 NUMBER OF SEQ ID NOS: 49
32 1700 SOFTWARE: FastSEQ for Windows Version 4.0
33 2100 SEQ ID NO: 1
36 2110 LENGTH: 1789
37 2120 TYPE: DNA
38 2130 ORGANISM: Homo sapiens
40 2400 SEQUENCE: 1
41  gattcatat gtgagatgtt accangggag tttcccgagg aaggatcttg cagcccgagt      60
42  ccccgaggata aactctgggg ttcatctccc ttcccttggt cactccacag tootcaggt      120
43  tctccaatcc aggggactcg ggcgcgggac gctgct atg gac gac att ttc act      174
44  cag tgc cgg gag ggc aac gca gtc gcc gtt cgc ctg tgg ctg gac aac      210
45  aag gag aac gac ctg aac cag ggg gac gtt cat ggc ttc tcc ccc ttg      270
46  aac tgg ccc ttc tga gag ggt agc tct gct gtg gtt gag atg ttg atc      318
47  atg cgg cgg gca cgg atc aat gta atg aac cgt ggg gat gac aac ccc      366
48  ctg cat ctg gca gcc aat cat gga cag cgt gat att gta cag aag cta      414
49  tgg cag taa aag gca gac atc aat gca gtg aat gaa cag ggg aat gtg      462
50  ccc ctg cag tat gcc cgt ttt tgg ggc caa gat caa gtg gca gag gac      510
51  cgg gtg gca aat ggg gcc att gtc agc atc tgt aac aag tat gga gag      558
52  atg cct gtg gac aaa gcc aac gca ccc ctg aga gag att ctc cga gag      606
53  cgg gca gaa aag atg gcc cag aat ctc aac cgt att cca tac aag gac      654
54  aca ttc tgg aag ggg acc acc tgc acc cgg ccc cga aat gga acc ctg      702
55  aac aaa cag tct ggc att gac ttc aaa cag att aac ttc ctg aag aag      750
56  ctc aac gag aat cag tct gga gat cta tgg aag ggc cgc tgg cag ggc      798
57  aat gac att gtc gtg aag gtg ctg aag gtt cga gac tgg agt aca agg      846
58  gag agc agg gac ttc aat gaa gag tgt ccc cgg ctc agg att ttc tgg      894
59  aat cca aat gtg ctc cca gtg cta ggt gcc tgc cag tct cca cct gct      942

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60 cct cat cct act ctc atc aca cac tgg atg cgg tat gga tcc ctc tac      990
61 aat gta cta cat gaa ggc acc aat ttc gtc gtg gac cag acc gag gct      1000
62 gtc aag ttt gct ttg gac atg gca agg ggc atg gcc ttc cta cac aca      1010
63 cta gag ccc ctc ctc cca cga cat gca ctc aat agc cgt agt gta atg      1020
64 att gat gag gac atg act gcc cga att agc atg gct gat gtc aag ttc      1030
65 tct ttc caa tgt cct ggt cgc atg tat gca cct gcc tgg gta gcc ccc      1040
66 gaa cct ctg cag aag aag cct gaa gac aca aac aga cgc tca gca gac      1050
67 atg tgg agt ttt gca gtg ctt ctg tgg gaa ctg gtg aca cgg gag gta      1060
68 ccc tct gct gac ctc tcc aat atg gag att gga atg aag gtg gca ttg      1070
69 gaa ggc ctt cgg cct acc atc cca cca ggt att tcc cct cat gtg tgt      1080
70 aag ctc atg aag atc tgc atg aat gaa gac cct gca aag cga ccc aaa      1090
71 ttt gac atg att gtg cct atc ctt gag aag atg cag gac aag      1100
72 taggactgga aggtccttgc ctgaactcca gaggtgtcgg gacatggttg ggggaatgca      1110
73 cctcaccaca gaagcaggcc tctggttgcc tccccgcct ccagtcattg tactaccaca      1120
74 gctcggggtc cctcccttc ccccatccct accactgtgc gcaagagggg cgggtccaga      1130
75 gcttctgcac tggccacatg gtgtctccca acatgggagg gatcagcccc gctgtccaca      1140
76 ataaagttaa ttatgaaaaa aaaaaa      1150
77 -L10- SEQ ID NO: 2
80 -L11- LENGTH: 452
81 -L12- TYPE: PRT
82 -L13- ORGANISM: Homo sapiens
84 -L400- SEQUENCE: 1
85 Met Asp Asp Ile Phe Thr Gln Cys Arg Glu Gly Asn Ala Val Ala Val
86 1 5 10 15
87 Arg Leu Trp Leu Asp Asn Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp
88 20 25 30
89 His Gly Phe Ser Pro Leu His Trp Ala Cys Arg Glu Gly Arg Ser Ala
90 35 40 45
91 Val Val Glu Met Leu Ile Met Arg Gly Ala Arg Ile Asn Val Met Asn
92 50 55 60
93 Arg Gly Asp Asp Thr Pro Leu His Leu Ala Ala Ser His Gly His Arg
94 65 70 75 80
95 Asp Ile Val Gln Lys Leu Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val
96 85 90 95
97 Asn Glu His Gly Asn Val Pro Leu His Tyr Ala Cys Phe Trp Gly Gln
98 100 105 110
99 Asp Gln Val Ala Glu Asp Leu Val Ala Asn Gly Ala Leu Val Ser Ile
100 115 120 125
101 Cys Asn Lys Tyr Gly Glu Met Pro Val Asp Lys Ala Lys Ala Pro Leu
102 130 135 140
103 Arg Glu Leu Leu Arg Glu Arg Ala Glu Lys Met Gly Gln Asn Leu Asn
104 145 150 155 160
105 Arg Ile Pro Tyr Lys Asp Thr Phe Trp Lys Gly Thr Thr Arg Thr Arg
106 165 170 175
107 Pro Arg Asn Gly Thr Leu Asn Lys His Ser Gly Ile Asp Phe Lys Gln
108 180 185 190
109 Leu Asn Phe Leu Thr Lys Leu Asn Glu Asn His Ser Gly Glu Leu Trp
110 195 200 205
111 Lys Gly Arg Trp Gln Gly Asn Asp Ile Val Val Lys Val Leu Lys Val

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113      210      215      220
112 Arg Asp Trp Ser Thr Arg Lys Ser Arg Asp Phe Asn Glu Glu Cys Pro
114 225      230      235      240
115 Arg Leu Arg Ile Phe Ser His Pro Asn Val Leu Pro Val Leu Gly Ala
116      245      250      255
117 Cys Gln Ser Pro Pro Ala Pro His Pro Thr Leu Ile Thr His Trp Met
118      260      265      270
119 Pro Tyr Gly Ser Leu Tyr Asn Val Leu His Glu Gly Thr Asn Phe Val
120      275      280      285
121 Val Asp Gln Ser Gln Ala Val Lys Phe Ala Leu Asp Met Ala Arg Gly
122      290      295      300
123 Met Ala Phe Leu His Thr Leu Gln Pro Leu Ile Pro Arg His Ala Leu
124 305      310      315      320
125 Asn Ser Arg Ser Val Met Ile Asp Glu Asp Met Thr Ala Arg Ile Ser
126      325      330      335
127 Met Ala Asp Val Lys Phe Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala
128      340      345      350
129 Pro Ala Trp Val Ala Pro Gln Ala Leu Gln Lys Lys Pro Glu Asp Thr
130      355      360      365
131 Asn Arg Arg Ser Ala Asp Met Trp Ser Phe Ala Val Leu Leu Trp Glu
132      370      375      380
133 Leu Val Thr Arg Glu Val Pro Phe Ala Asp Leu Ser Asn Met Glu Ile
134 385      390      395      400
135 Gly Met Lys Val Ala Leu Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly
136      405      410      415
137 Ile Ser Pro His Val Cys Lys Leu Met Lys Ile Cys Met Asn Glu Asp
138      420      425      430
139 Pro Ala Lys Arg Pro Lys Phe Asp Met Ile Val Pro Ile Leu Glu Lys
140      435      440      445
141 Met Gln Asp Lys
142      450
145 <110> SEQ ID NO: 3
146 <211> LENGTH: 19
147 <212> TYPE: DNA
148 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 3
151 agtccatagc aggtcccg 19
153 <110> SEQ ID NO: 4
154 <211> LENGTH: 18
155 <212> TYPE: DNA
156 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 4
159 accctggttg cagtccac 18
161 <110> SEQ ID NO: 5
162 <211> LENGTH: 19
163 <212> TYPE: DNA
164 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 5
167 cctttccgg ggaactccc 19

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169 <210> SEQ ID NO: 6
170 <211> LENGTH: 19
171 <212> TYPE: DNA
172 <213> ORGANISM: Homo sapiens
173 <400> SEQUENCE: 6
175 ggggactcag gctacaggc 19
177 <210> SEQ ID NO: 7
178 <211> LENGTH: 19
179 <212> TYPE: DNA
180 <213> ORGANISM: Homo sapiens
181 <400> SEQUENCE: 7
183 ggtttatctc cgggactcc 19
185 <210> SEQ ID NO: 8
186 <211> LENGTH: 19
187 <212> TYPE: DNA
188 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 8
191 ggggagggag atgagaccc 19
193 <210> SEQ ID NO: 9
194 <211> LENGTH: 19
195 <212> TYPE: DNA
196 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 9
199 ggcctgaggc tgtcagagta 19
201 <210> SEQ ID NO: 10
202 <211> LENGTH: 18
203 <212> TYPE: DNA
204 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 10
207 ggggaagcct gaggactg 18
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 19
211 <212> TYPE: DNA
212 <213> ORGANISM: Homo sapiens
213 <400> SEQUENCE: 11
215 gattgaaat gtgttccat 19
217 <210> SEQ ID NO: 12
218 <211> LENGTH: 19
219 <212> TYPE: DNA
220 <213> ORGANISM: Homo sapiens
221 <400> SEQUENCE: 12
223 aatgggcact cagttggcc 19
225 <210> SEQ ID NO: 13
226 <211> LENGTH: 19
227 <212> TYPE: DNA
228 <213> ORGANISM: Homo sapiens
229 <400> SEQUENCE: 13
231 tctgtctcag caataggcg 19
233 <210> SEQ ID NO: 14

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334 <211> LENGTH: 19
335 <212> TYPE: DNA
336 <213> ORGANISM: Homo sapiens
337 <400> SEQUENCE: 14
338 tgggtgaggt cgttcctccg 19
341 <210> SEQ ID NO: 15
342 <211> LENGTH: 19
343 <212> TYPE: DNA
344 <213> ORGANISM: Homo sapiens
345 <400> SEQUENCE: 15
346 gaagccatga tcgtccccc 19
347 <210> SEQ ID NO: 16
348 <211> LENGTH: 19
349 <212> TYPE: DNA
350 <213> ORGANISM: Homo sapiens
351 <400> SEQUENCE: 16
352 cagcccccgt gaaagagg 19
353 <210> SEQ ID NO: 17
354 <211> LENGTH: 19
355 <212> TYPE: DNA
356 <213> ORGANISM: Homo sapiens
357 <400> SEQUENCE: 17
358 cggccctctc gccaggcc 19
359 <210> SEQ ID NO: 18
360 <211> LENGTH: 19
361 <212> TYPE: DNA
362 <213> ORGANISM: Homo sapiens
363 <400> SEQUENCE: 18
364 ccaacgcara cgggcctc 19
365 <210> SEQ ID NO: 19
366 <211> LENGTH: 19
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
369 <400> SEQUENCE: 19
370 cggcatgata aacatctc 18
371 <210> SEQ ID NO: 20
372 <211> LENGTH: 18
373 <212> TYPE: DNA
374 <213> ORGANISM: Homo sapiens
375 <400> SEQUENCE: 20
376 ttgatccctg cccccgc 18
377 <210> SEQ ID NO: 21
378 <211> LENGTH: 19
379 <212> TYPE: DNA
380 <213> ORGANISM: Homo sapiens
381 <400> SEQUENCE: 21
382 cctcccacg qttcattac 19
383 <210> SEQ ID NO: 22
384 <211> LENGTH: 19

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VERIFICATION SUMMARY

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